

U.S. Patent Application No. 10/611,414
Amendment Dated February 14, 2008
In Response to Office Action of November 16, 2007

Amendments to the Claims

This listing of claims will replace all prior versions, and listings, of claims in the application:

Listing of claims:

1. (Currently Amended) A method for allelic classification, the method comprising:

acquiring intensity information for each of a plurality of samples wherein the intensity information for each sample of the plurality of samples comprises a first intensity component representing the detected emission of a first probe associated with specific for a first allele of a gene and a second intensity component representing the detected emission of a second probe associated with specific for a second allele of the gene;

forming a plurality of data sets from the intensity information, such that each data set comprises the first intensity component and the second intensity component from a respective one of the plurality of samples:

grouping the plurality of data sets into one or more data clusters by evaluating at least the relationship between the first intensity component and the second intensity component for each of the plurality of samples to identify one or more data clusters, wherein each data cluster identifying a unique represents a discrete allelic classification comprising one of a discrete combination of alleles selected from neither the first allele nor the second allele, a homozygous allelic combination comprising the first allele alone, a homozygous allelic combination comprising the second allele alone, and or a

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heterozygous allelic combination comprising both the first allele and the second allele;

defining bounds for each of the one or more data clusters;

generating a likelihood model that predicts the probability that an allelic combination of a selected sample from the plurality of samples will reside within the bounds of a particular data cluster of the one or more data clusters, based upon the intensity information of the selected sample;

applying the likelihood model to the intensity information of each of the plurality of samples to identify the associated allelic classification for of each corresponding sample of the plurality of samples; and

outputting the allelic classification of each of the plurality of samples to at least one of a user, a database, an application, and an instrument and a display.

2. (Original) The method of claim 1, wherein the likelihood model comprises a model-fit probability assessment that estimates confidence in the likelihood model itself and assesses how well a selected sample and its respective intensity information fit the model.

3. (Original) The method of claim 1, wherein the likelihood model comprises an in-class probability assessment that estimates the probability that a selected cluster identifies a selected sample and its respective intensity information.

4. (Original) The method of claim 1, wherein the likelihood model comprises an a posteriori probability assessment that estimates the probability of a selected sample and

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its respective intensity information belonging to an assigned cluster.

5. (Previously Presented) The method of claim 1, wherein the one or more data clusters comprise at least three discrete data clusters each associated with a different combination selected from neither the first allele nor the second allele, the first allele alone, the second allele alone, and both the first allele and the second allele.
6. (Currently Amended) The method of claim 1, wherein the at least one data cluster comprises a cluster type associated with representing a first homozygous allelic classification.
7. (Currently Amended) The method of claim 1, wherein the at least one data cluster comprises a cluster type associated with representing a first heterozygous allelic classification.
8. (Currently Amended) The method of claim 1, wherein the at least one data cluster comprises a cluster type associated with representing a second homozygous allelic classification.
9. (Original) The method of claim 1, wherein the allelic classification is used to perform a mutational analysis of one or more samples.
10. (Original) The method of claim 1, wherein the allelic classification is used to

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perform a single nucleotide polymorphism analysis of one or more samples.

11. (Currently Amended) The method of claim 1, wherein ~~the~~ a genotype for one or more samples is identified by performing the allelic classification.

12. (Currently Amended) The method of claim 1, wherein the intensity information for the plurality of ~~clusters~~ samples is normalized.

13. (Previously presented) The method of claim 1, wherein the plurality of samples comprise at least one control sample and associated intensity information that is used for the purposes of sample scaling.

14. (Original) The method of claim 1, wherein the likelihood model is generated in an iterative manner to refine the likelihood model.

15. (Original) The method of claim 14, wherein two or more iterations are used to generate a refined likelihood model.

16. (Canceled)

17. (Original) The method of claim 14, wherein refinement of the likelihood model comprises performing a data resampling operation wherein a subset of the plurality of samples are used to generate the refined likelihood model.

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18. (Canceled)

19. (Previously presented) The method of claim 1, wherein the intensity information for each sample is acquired from an amplification protocol.

20. (Previously presented) The method of claim 19, wherein the amplification protocol comprises a Taqman or SNPlex protocol.

21. (Original) The method of claim 1, wherein the intensity information for each sample is acquired from an array-based detection protocol.

22. – 83. (Canceled)

84. (Previously Presented) The method of claim 1, further comprising acquiring a plot of the intensity information, the plot comprising a first axis corresponding to the first intensity component and a second axis corresponding to the second intensity component.

85. (Previously Presented) The method of claim 84, wherein the one or more data clusters each comprise groupings of data points defined by the first intensity component and the second intensity component in a discrete area of the plot.